Relocation and co-regulated gene expression patterns in Fusarium graminearum

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Genome comparisons between closely related species often show non-conserved regions across chromosomes. Some of them are located in specific regions of chromosomes and some are even confined to one or more entire chromosomes. The origin and biological relevance of these non-conserved regions are still largely unknown. The genome of *Fusarium graminearum* genome was studied to elucidate the significance of non-conserved regions. In the genome of *F. graminearum* harbours thirteen non-conserved regions dispersed over all of the four chromosomes. Using RNA-Seq data from the mycelium of *F. graminearum*, we found weakly expressed regions on all of the four chromosomes that exactly matched with non-conserved regions. Comparison of gene expression between two different developmental stages (conidia and mycelium) showed that the expression of genes in conserved regions is stable, while gene expression in non-conserved regions is much more influenced by the developmental stage. In addition, genes involved in the production of secondary metabolites and secreted proteins are enriched in non-conserved regions, suggesting that these regions could also be important for adaptations to new environments, including adaptation to new hosts. Finally, we found evidence that non-conserved regions are generated by sequestration of genes from multiple locations. Gene relocations may lead to clustering of genes with similar expression patterns or similar biological functions, which was clearly exemplified by the *PKS2* gene cluster. Our results showed that chromosomes can be functionally divided into conserved and non-conserved regions, and both could have specific and distinct roles in genome evolution and regulation of gene expression.

Reference:

Relocation of genes generates non-conserved chromosomal segments in *Fusarium graminearum* that show distinct and co-regulated gene expression patterns. C Zhao, C Waalwijk, PJGM de Wit, D Tang, T van der Lee. BMC genomics 15 (1), 191